

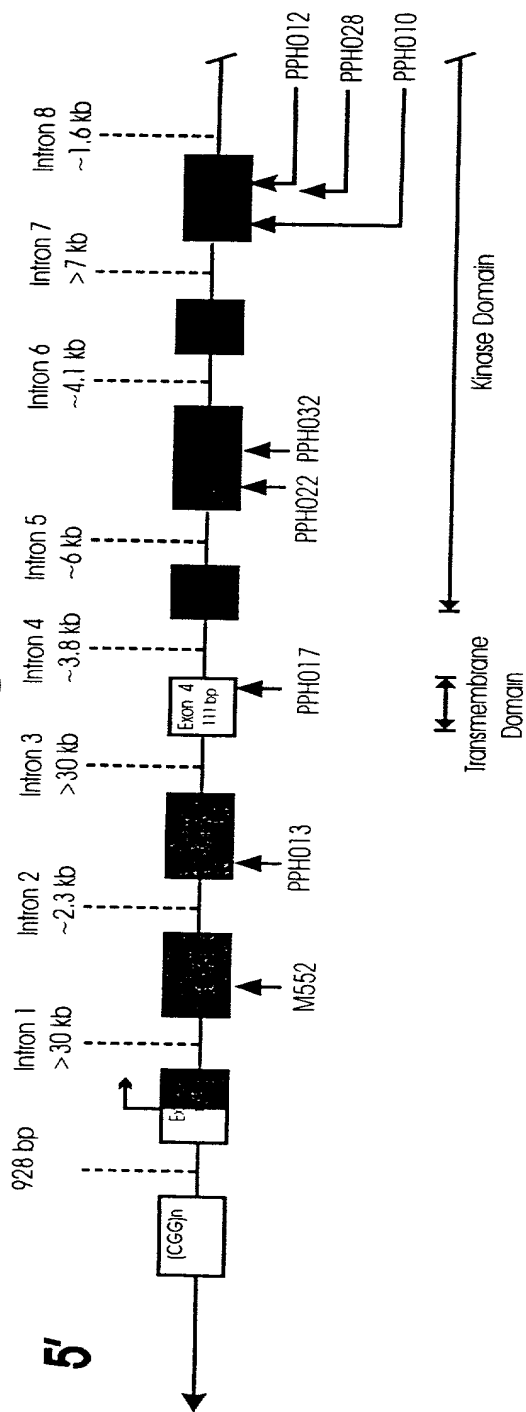
Figure 1-1

EXON (SIZE)	EXON 3'		INTRON (SIZE)		EXON 5'
EXON 1 (>460 bp)	GCT G Ala A	gtgagtagctccggc...	intron 1 (>30 kb)	..tttcctttatatttag	CT TCG la Ser
EXON 2 (171 bp)	CAA G Gln G	gcaagtgatactttc...	intron 2 (~2.3 kb)	..catattgatttatag	GA TAT ly Cys
EXON 3 (171 bp)	CTC A Leu S	gtaagtaaaagtaacc...	intron 3 (>30 kb)	..tttgttttctcttttag	GT CCA er Pro
EXON 4 (111 bp)	ACA G Thr G	gtaaaaattaccatt...	intron 4 (~3.8 kb)	..ttcctgttctttatag	GA GAC ly Asp
EXON 5 (92 bp)	TTG GAG Leu Glu	gtaagtttgccgtta...	intron 5 (~6 kb)	..ttaaaacacttgacag	CTG ATT Leu Ile
EXON 6 (231 bp)	CCC AAT Pro Asn	gtaagttcttctcatag...	intron 6 (~4.1 kb)	..ttttcctcttatatag	GGA TCT Gly Ser
EXON 7 (115 bp)	GCA G Gly A	gtaagatagtcaata...	intron 7 (>7 kb)	..aaattatccaaacag	AT CAT sp His
EXON 8 (161 bp)	AGC GAG Ser Glu	gtgagtgatatacaaa...	intron 8 (~1.6 kb)	..actctaatttatcag	GTT GGC Val Gly
EXON 9 (148 bp)	CCA G Pro G	gtaaaaactactgtc...	intron 9 (>9.7 kb)	..tctacaaatccacag	GG GAA ly Glu
EXON 10 (137 bp)	AGC CTG Ser Leu	gtaagaaaaaaactaa...	intron 10 (>5 kb)	..tactttgtctttacag	GCA GTG Ala Val
EXON 11 (173 bp)	GAA CG	gtaagaccctaagg...	intron 11 (>20 kb)	..ctttctttctttaag	C AAC

Figure 1-2

EXON 12 (1280 bp)	Glu Ar	
	CAG A	gtaagtggaggatc..
	Gln I	intron 12 (~1.8 kb)
EXON 13 (>251 bp)		..cacttttattttcag
		g Asn
		TA GGT
		le Gly

Figure 2



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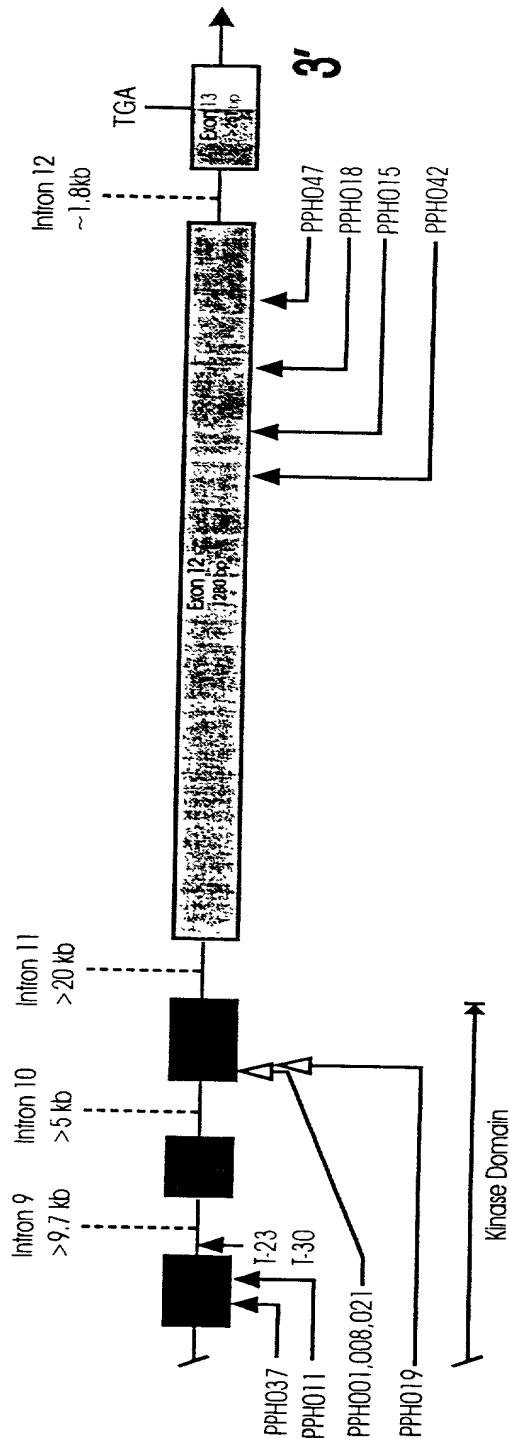


Figure 3

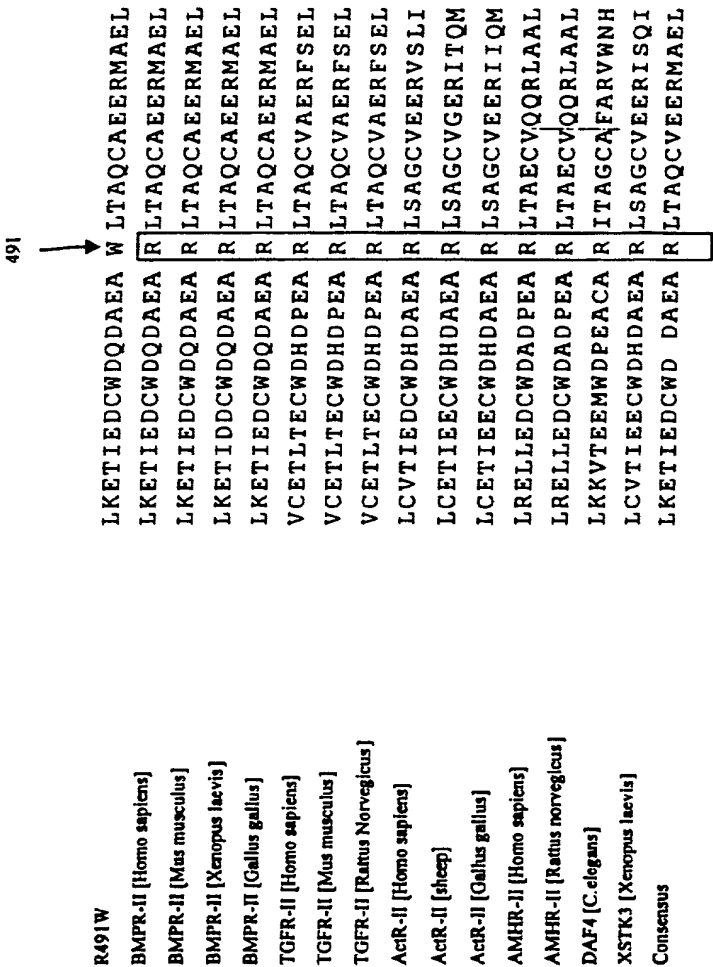


Figure 4

Family #	#A/#C/#U	Exon #	DNA Sequence Variation	Protein Sequence Variation
PPH001, 008 and 021	4/5/13	11	1471C>T	R491W
PPH010	2/0/1	8	1099-1103delGGGA	E368fsX1
PPH015	6/1/8	12	2579delT	N861fsX10
PPH017	3/0/6	4	507-510delCTTTinsAAA	C169X
PPH018	3/2/4	12	2617C>T	R873X
PPH019	1/0/5*	11	1472G>A	R491Q
PPH022	2/0/0	6	690-691delAGinsT	K230fsX21
PPH011		9	1248-1251delATT	F417X
PPH012		8	994C>T	R332X
PPH013		3	295T>C	C99R
PPH028		8	1097delG	P366fsX8
PPH032		6	727G>T	E243X
PPH037		9	1214delA	D405fsX6
PPH042		12	2441-2442delAC	H814fsX2
PPH047		12	2695C>T	R899X
M552		2	189-209del21	Del 64-70(STCYGLW)
PPH045		3	296G>A	C99Y
PPH052		3	250T>C	C84R
PPH67-6701		8	1040G>A	C347Y

Figure 5-1

+1	Met	Thr	Ser	Ser	Leu	Gln	Arg	Pro	Trp	Arg	Val	Pro	Trp	Leu	Pro	Trp	Thr	
1	ATGACTTCCT	CGCTGCAGCG	GCCCTGGCGG	GTGCCCTGGC	TACCATGGAC													
	TACTGAAGGA	GCGACGTCGC	CGGGACCGCC	CACGGGACCG	ATGGTACCTG													
+1	Thr	Ile	Leu	Leu	Val	Ser	Thr	Ala	Ala	Ala	Ser	Gln	Asn	Gln	Glu	Arg	Leu	Cys
51	CATCCTGCTG	GTCAGCACTG	CGGCTGCTTC	GCAGAAATCAA	GAACGGCTAT													
	GTAGGACGAC	CAGTCGTGAC	GCCGACGAAG	CGTCTTAGTT	CTTGCCGATA													
+1	Cys	Ala	Phe	Lys	Asp	Pro	Tyr	Gln	Gln	Asp	Leu	Gly	Ile	Gly	Glu	Ser	Arg	
101	GTGCGTTTAA	AGATCCGTAT	CAGCAAGACC	TTGGGATAGG	TGAGAGTAGA													
	CACGCAAATT	TCTAGGCATA	GTCGTTCTGG	AACCCTATCC	ACTCTCATCT													
+1	Ile	Ser	His	Glu	Asn	Gly	Thr	Ile	Leu	Cys	Ser	Lys	Gly	Ser	Thr	Cys	Tyr	
151	ATCTCTCATG	AAAATGGGAC	AATATTATGC	TCGAAAGGTA	GCACCTGCTA													
	TAGAGAGTAC	TTTTACCCTG	TTATAATACG	AGCTTTCCAT	CGTGGACGAT													
+1	Tyr	Gly	Leu	Trp	Glu	Lys	Ser	Lys	Gly	Asp	Ile	Asn	Leu	Val	Lys	Gln	Gly	Cys
201	TGGCCTTTGG	GAGAAATCAA	AAGGGGACAT	AAATCTTGTA	AAACAAGGAT													
	ACCGGAAACC	CTCTTTAGTT	TTCCCTGTGA	TTTAGAACAT	TTTGTTCCTA													
+1	Cys	Trp	Ser	His	Ile	Gly	Asp	Pro	Gln	Glu	Cys	His	Tyr	Glu	Glu	Cys	Val	
251	GTTGGTCTCA	CATTGGAGAT	CCCCAAGAGT	GTCACATGA	AGAATGTGTA													
	CAACCAGAGT	GTAACCTCTA	GGGGTTCTCA	CAGTGATACT	TCTTACACAT													
+1	Val	Thr	Thr	Thr	Pro	Pro	Ser	Ile	Gln	Asn	Gly	Thr	Tyr	Arg	Phe	Cys	Cys	
301	GTAACATCCA	CTCCTCCCTC	AATTCAGAAT	GGAACATACC	GTTTCTGCTG													
	CATTGATGGT	GAGGAGGGAG	TTAAGTCTTA	CCTTGTATGG	CAAAGACGAC													
+1	Cys	Cys	Ser	Thr	Asp	Leu	Cys	Asn	Val	Asn	Phe	Thr	Glu	Asn	Phe	Pro	Pro	Pro
351	TTGTAGCACA	GATTATGTGA	ATGTCAACTT	TACTGAGAAT	TTTCCACCTC													
	AACATCGTGT	CTAAATACAT	TACAGTTGAA	ATGACTCTTA	AAAGGTGGAG													
+1	Pro	Asp	Thr	Thr	Pro	Leu	Ser	Pro	Pro	His	Ser	Phe	Asn	Arg	Asp	Glu	Thr	
401	CTGACACAAC	ACCACTCAGT	CCACCTCATT	CATTTAACCG	AGATGAGACA													
	GACTGTGTTG	TGGTGAGTCA	GGTGGAGTAA	GTAAATTGGC	TCTACTCTGT													
+1	Ile	Ile	Ile	Ala	Leu	Ala	Ser	Val	Ser	Val	Leu	Ala	Val	Leu	Ile	Val	Ala	
451	ATAATCATTG	CTTTGGCATC	AGTCTCTGTA	TTAGCTGTTT	TGATAGTTGC													
	TATTAGTAAC	GAAACCGTAG	TCAGAGACAT	AATCGACAAA	ACTATCAACG													
+1	Ala	Leu	Cys	Phe	Gly	Tyr	Arg	Met	Leu	Thr	Gly	Asp	Arg	Lys	Gln	Gly	Leu	His
501	CTTATGCTTT	GGATACAGAA	TGTTGACAGG	AGACCGTAAA	CAAGGTCTTC													
	GAATACGAAA	CCTATGTCTT	ACAACTGTCC	TCTGGCATT	GTTCCAGAAG													
+1	His	Ser	Met	Asn	Met	Met	Glu	Ala	Ala	Ala	Ser	Glu	Pro	Ser	Leu	Asp	Leu	
551	ACAGTATGAA	CATGATGGAG	GCAGCAGCAT	CCGAACCTC	TCTTGATCTA													
	TGTCATACTT	GTAACCTC	CGTCGTCGTA	GGCTTGGGAG	AGAACTAGAT													
+1	Asp	Asn	Leu	Lys	Leu	Leu	Glu	Leu	Ile	Gly	Arg	Gly	Arg	Tyr	Gly	Ala	Val	
601	GATAATCTGA	AACGTGTGGA	GCTGATTGGC	CGAGGTGCGAT	ATGGAGCAGT													
	CTATTAGACT	TTGACAACCT	CGACTAACCG	GCTCCAGCTA	TACCTCGTCA													
+1	Val	Tyr	Lys	Gly	Ser	Leu	Asp	Glu	Arg	Pro	Val	Ala	Val	Lys	Val	Phe	Ser	Phe
651	ATATAAAGGC	TCCTTGGATG	AGCGTCCAGT	TGCTGTAAAA	GTGTTTTCCT													
	TATATTTCGG	AGGAACCTAC	TCGCAGGTCA	ACGACATTTT	CACAAAAGGA													
+1	Phe	Ala	Asn	Arg	Gln	Asn	Phe	Ile	Asn	Glu	Lys	Asn	Ile	Tyr	Arg	Val	Pro	
701	TTGCAAACCG	TCAGAAATTTT	ATCAACGAAA	AGAACATTTA	CAGAGTGCCT													
	AACGTTTGGC	AGTCTTAAAA	TAGTTGCTTT	TCTTGTAAT	GTCTCACGGA													
+1	Leu	Met	Glu	His	Asp	Asn	Ile	Ala	Arg	Phe	Ile	Val	Gly	Asp	Glu	Arg	Val	
751	TTGATGGAAC	ATGACAACAT	TGCCCGCTTT	ATAGTTGGAG	ATGAGAGAGT													
	AACTACCTTG	TACTGTTGTA	ACGGGCGAAA	TATCAACCTC	TACTCTCTCA													

Figure 5-2

+1	Val	Thr	Ala	Asp	Gly	Arg	Met	Glu	Tyr	Leu	Leu	Val	Met	Glu	Tyr	Tyr	Pro	Asn
801	CACTGCAGAT	GGACGCATGG	AATATTTGCT	TGTGATGGAG	TACTATCCCA	GTGACGTCTA	CCTGCGTACC	TTATAAACGA	ACACTACCTC	ATGATAGGGT								
+1	Asn	Gly	Ser	Leu	Qs	Lys	Tyr	Leu	Ser	Leu	His	Thr	Ser	Asp	Trp	Val	Ser	
851	ATGGATCTTT	ATGCAAGTAT	TTAAGTCTCC	ACACAAGTGA	CTGGGTAAAGC	TACCTAGAAA	TACGTTTATA	AATTCAGAGG	TGTGTTCACT	GACCCATTCTG								
+1	Ser	Qs	Arg	Leu	Ala	His	Ser	Val	Thr	Arg	Gly	Leu	Ala	Tyr	Leu	His	Thr	
901	TCTTGCCGTC	TTGCTCATTG	TGTTACTAGA	GGACTGGCTT	ATCTTCACAC	AGAACGGCAG	AACGAGTAA	ACAATGATCT	CCTGACCGAA	TAGAAGTGTG								
+1	Thr	Glu	Leu	Pro	Arg	Gly	Asp	His	Tyr	Lys	Pro	Ala	Ile	Ser	His	Arg	Asp	Leu
951	AGAATTACCA	CGAGGAGATC	ATTATAAACC	TGCAATTTCC	CATCGAGATT	TCTTAATGGT	GCTCCTCTAG	TAATATTTGG	ACGTAAAGG	GTAGCTCTAA								
+1	Leu	Asn	Ser	Arg	Asn	Val	Leu	Val	Lys	Asn	Asp	Gly	Thr	Qs	Val	Ile	Ser	
1001	TAAACAGCAG	AAATGTCCTA	GTGAAAAATG	ATGGAACCTG	TGTTATTAGT	ATTTGTGCTC	TTTACAGGAT	CACTTTTTAC	TACCTTGGAC	ACAATAATCA								
+1	Asp	Phe	Gly	Leu	Ser	Met	Arg	Leu	Thr	Gly	Asn	Arg	Leu	Val	Arg	Pro	Gly	
1051	GACTTTGGAC	TGTCCATGAG	GCTGACTGGA	AATAGACTGG	TGCGCCGAGG	CTGAAACCTG	ACAGGTACTC	CGACTGACCT	TTATCTGACC	ACGCGGGTCC								
+1	Gly	Glu	Glu	Asp	Asn	Ala	Ala	Ile	Ser	Glu	Val	Gly	Thr	Ile	Arg	Tyr	Met	Ala
1101	GGAGGAAGAT	AATGCAGCCA	TAAGCGAGGT	TGGCACTATC	AGATATATGG	CCTCCTTCTA	TTACGTCTGGT	ATTGCTCTCA	ACCGTGATAG	TCTATATACC								
+1	Ala	Pro	Glu	Val	Leu	Glu	Gly	Ala	Val	Asn	Leu	Arg	Asp	Qs	Glu	Ser	Ala	
1151	CACCAGAAGT	GCTAGAAGGA	GCTGTGAACT	TGAGGGACTG	TGAATCAGCT	GTGGTCTTCA	CGATCTTCCT	CGACACTTGA	ACTCCCTGAC	ACTTAGTCGA								
+1	Leu	Lys	Gln	Val	Asp	Met	Tyr	Ala	Leu	Gly	Leu	Ile	Tyr	Trp	Glu	Ile	Phe	
1201	TTGAAACAAG	TAGACATGTA	TGCTCTTGGA	CTAATCTATT	GGGAGATATT	AACCTTGTTC	ATCTGTACAT	ACGAGAACCT	GATTAGATAA	CCCTCTATAA								
+1	Phe	Met	Arg	Qs	Thr	Asp	Leu	Phe	Pro	Gly	Glu	Ser	Val	Pro	Glu	Tyr	Gln	Met
1251	TATGAGATGT	ACAGACCTCT	TCCCAGGGGA	ATCCGTACCA	GAGTACCAGA	ATACTCTACA	TGTCTGGAGA	AGGGTCCCCCT	TAGGCATGGT	CTCATGGTCT								
+1	Met	Ala	Phe	Gln	Thr	Glu	Val	Gly	Asn	His	Pro	Thr	Phe	Glu	Asp	Met	Gln	
1301	TGGCTTTTCA	GACAGAGGTT	GGAAACCATC	CCACTTTTGA	GGATATGCAG	ACCGAAAAGT	CTGTCTCCAA	CCTTTGGTAG	GGTGAAAACCT	CCTATACGTC								
+1	Val	Leu	Val	Ser	Arg	Glu	Lys	Gln	Arg	Pro	Lys	Phe	Pro	Glu	Ala	Trp	Lys	
1351	GTTCTCGTGT	CTAGGGAAAA	ACAGAGACCC	AAGTTCCCAG	AAGCCTGGAA	CAAGAGCACA	GATCCCTTTT	TGTCTCTGGG	TTCAAGGGTC	TTCGGACCTT								
+1	Lys	Glu	Asn	Ser	Leu	Ala	Val	Arg	Ser	Leu	Lys	Glu	Thr	Ile	Glu	Asp	Qs	Trp
1401	AGAAAATAGC	CTGGCAGTGA	GGTCACTCAA	GGAGACAATC	GAAGACTGTT	TCTTTTATCG	GACCGTCACT	CCAGTGAGTT	CCTCTGTAG	CTTCTGACAA								
+1	Trp	Asp	Gln	Asp	Ala	Glu	Ala	Arg	Leu	Thr	Ala	Gln	Qs	Ala	Glu	Glu	Arg	
1451	GGGACCAGGA	TGCAGAGGCT	CGGCTTACTG	CACAGTGTGC	TGAGGAAAGG	CCCTGGTCTC	ACGTCTCCGA	GCCGAATGAC	GTGTCACACG	ACTCCTTTCC								
+1	Met	Ala	Glu	Leu	Met	Met	Ile	Trp	Glu	Arg	Asn	Lys	Ser	Val	Ser	Pro	Thr	
1501	ATGGCTGAAC	TTATGATGAT	TTGGGAAAGA	AACAAATCTG	TGAGCCCAAC	TACCGACTTG	AATACTACTA	AACCCCTTCT	TTGTTTAGAC	ACTCGGGTTG								
+1	Thr	Val	Asn	Pro	Met	Ser	Thr	Ala	Met	Gln	Asn	Glu	Arg	Asn	Leu	Ser	His	Asn
1551	AGTCAATCCA	ATGTCTACTG	CTATGCAGAA	TGAACGCAAC	CTGTACATA	TCAGTTAGGT	TACAGATGAC	GATACGTCTT	ACTTGCGTTG	GACAGTGTAT								

Figure 5-3

+1	Asn	Arg	Arg	Val	Pro	Lys	Ile	Gly	Pro	Tyr	Pro	Asp	Tyr	Ser	Ser	Ser	Ser
1601	ATAGGCGTGT	GCCAAAAATT	GGTCCTTATC	CAGATTATTC	TTCCTCCTCA	TATCCGCACA	CGGTTTTTAA	CCAGGAATAG	GTCTAATAAG	AAGGAGGAGT							
+1	Tyr	Ile	Glu	Asp	Ser	Ile	His	His	Thr	Asp	Ser	Ile	Val	Lys	Asn	Ile	Ser
1651	TACATTGAAG	ACTCTATCCA	TCATACTGAC	AGCATCGTGA	AGAATATTTT	ATGTAACTTC	TGAGATAGGT	AGTATGACTG	TCGTAGCACT	TCTTATAAAG							
+1	Ser	Ser	Glu	His	Ser	Met	Ser	Ser	Thr	Pro	Leu	Thr	Ile	Gly	Glu	Lys	Asn
1701	CTCTGAGCAT	TCTATGTCCA	GCACACCTTT	GACTATAGGG	GAAAAAACC	GAGACTCGTA	AGATACAGGT	CGTGTGGAAA	CTGATATCCC	CTTTTTTTGG							
+1	Arg	Asn	Ser	Ile	Asn	Tyr	Glu	Arg	Gln	Gln	Ala	Gln	Ala	Arg	Ile	Pro	Ser
1751	GAAATTCAAT	TAACTATGAA	CGACAGCAAG	CACAAGCTCG	AATCCCCAGC	CTTTAAGTTA	ATTGATACTT	GCTGTCGTTC	GTGTTTCGAGC	TTAGGGGTCTG							
+1	Pro	Glu	Thr	Ser	Val	Thr	Ser	Leu	Ser	Thr	Asn	Thr	Thr	Thr	Thr	Asn	Thr
1801	CCTGAAACAA	GTGTCACCAG	CCTCTCCACC	AACACAACAA	CCACAAACAC	GGACTTTGTT	CACAGTGGTC	GGAGAGGTGG	TTGTGTTGTT	GGTGTGTTGTG							
+1	Thr	Thr	Gly	Leu	Thr	Pro	Ser	Thr	Gly	Met	Thr	Thr	Ile	Ser	Glu	Met	Pro
1851	CACAGGACTC	ACGCCAAGTA	CTGGCATGAC	TACTATATCT	GAGATGCCAT	GTGTCTGAG	TGCGGTTCAT	GACCGTACTG	ATGATATAGA	CTCTACGGTA							
+1	Tyr	Pro	Asp	Glu	Thr	Asn	Leu	His	Thr	Thr	Asn	Val	Ala	Gln	Ser	Ile	Gly
1901	ACCCAGATGA	AACAAATCTG	CATACCACAA	ATGTTGCACA	GTCAATTGGG	TGGGTCTACT	TTGTTTAGAC	GTATGGTGTT	TACAACGTGT	CAGTTAAACC							
+1	Pro	Thr	Pro	Val	Gln	Leu	Gln	Leu	Thr	Glu	Glu	Asp	Leu	Glu	Thr	Asn	Lys
1951	CCAACCCCTG	TCTGCTTACA	GCTGACAGAA	GAAGACTTGG	AAACCAACAA	GGTTGGGGAC	AGACGAATGT	CGACTGTCTT	CTTCTGAACC	TTGGTTGTTT							
+1	Lys	Leu	Asp	Pro	Lys	Glu	Val	Asp	Lys	Asn	Leu	Lys	Glu	Ser	Ser	Asp	Glu
2001	GCTAGACCCA	AAAGAAGTTG	ATAAGAACCT	CAAGGAAAGC	TCTGATGAGA	CGATCTGGGT	TTTCTTCAAC	TATTCTTGGA	GTTCCTTTCG	AGACTACTCT							
+1	Asn	Leu	Met	Glu	His	Ser	Leu	Lys	Gln	Phe	Ser	Gly	Pro	Asp	Pro	Leu	Ser
2051	ATCTCATGGA	GCACTCTCTT	AAACAGTTCA	GTGGCCCAAG	CCCCTGAGC	TAGAGTACCT	CGTGAGAGAA	TTTGTCAAGT	CACCGGGTCT	GGGTGACTCG							
+1	Ser	Thr	Ser	Ser	Ser	Leu	Leu	Tyr	Pro	Leu	Ile	Lys	Leu	Ala	Val	Glu	Ala
2101	AGTACTAGTT	CTAGCTTGCT	TTACCCACTC	ATAAACTTGG	CAGTAGAAGC	TCATGATCAA	GATCGAACGA	AATGGGTGAG	TATTTTGAAC	GTCATCTTCG							
+1	Ala	Thr	Gly	Gln	Gln	Asp	Phe	Thr	Gln	Thr	Ala	Asn	Gly	Gln	Ala	Gln	Leu
2151	AACTGGACAG	CAGGACTTCA	CACAGACTGC	AAATGGCCAA	GCATGTTTGA	TTGACCTGTC	GTCCTGAAGT	GTGTCTGACG	TTTACCGGTT	CGTACAAACT							
+1	Ile	Pro	Asp	Val	Leu	Pro	Thr	Gln	Ile	Tyr	Pro	Leu	Pro	Lys	Gln	Gln	Asn
2201	TTCCTGATGT	TCTGCCTACT	CAGATCTATC	CTCTCCCCAA	GCAGCAGAAC	AAGGACTACA	AGACGGATGA	GTCTAGATAG	GAGAGGGGTT	CGTCGTCTTG							
+1	Leu	Pro	Lys	Arg	Pro	Thr	Ser	Leu	Pro	Leu	Asn	Thr	Lys	Asn	Ser	Thr	Lys
2251	CTTCCCAAGA	GACCTACTAG	TTTGCCTTTG	AACACCAAAA	ATTCAACAAA	GAAGGGTTCT	CTGGATGATC	AAACGGAAAAC	TTGTGGTTTT	TAAGTTGTTT							
+1	Lys	Glu	Pro	Arg	Leu	Lys	Phe	Gly	Ser	Lys	His	Lys	Ser	Asn	Leu	Lys	Gln
2301	AGAGCCCCGG	CTAAAATTTG	GCAGCAAGCA	CAAATCAAAC	TTGAAACAAG	TCTCGGGGCC	GATTTTAAAC	CGTCGTTTCG	GTTTAGTTTG	AACTTTGTTC							
+1	Val	Glu	Thr	Gly	Val	Ala	Lys	Met	Asn	Thr	Ile	Asn	Ala	Ala	Glu	Pro	His
2351	TCGAAACTGG	AGTTGCCAAG	ATGAATACAA	TCAATGCAGC	AGAACCTCAT	AGCTTTGACC	TCAACGGTTC	TACTTATGTT	AGTTACGTCG	TCTTGAGTA							

Figure 5-4

+1	Val	Val	Thr	Val	Thr	Met	Asn	Gly	Val	Ala	Gly	Arg	Asn	His	Ser	Val	Asn
2401	GTGGTGACAG	TCACCATGAA	TGGTGTGGCA	GGTAGAAACC	ACAGTGTAA	CACCACTGTC	AGTGGTACTT	ACCACACCGT	CCATCTTTGG	TGTCACAATT							
+1	Asn	Ser	His	Ala	Ala	Thr	Thr	Gln	Tyr	Ala	Asn	Arg	Thr	Val	Leu	Ser	Gly
2451	CTCCCATGCT	GCCACAACCC	AATATGCCAA	TAGGACAGTA	CTATCTGGCC	GAGGGTACGA	CGGTGTTGGG	TTATACGGTT	ATCCTGTCAT	GATAGACCGG							
+1	Gln	Thr	Thr	Asn	Ile	Val	Thr	His	Arg	Ala	Gln	Glu	Met	Leu	Gln	Asn	Gln
2501	AAACAACCAA	CATAGTGACA	CATAGGGCCC	AAGAAATGTT	GCAGAATCAG	TTTGTGGTT	GTATCACTGT	GTATCCCGGG	TTCTTTACAA	CGTCTTAGTC							
+1	Phe	Ile	Gly	Glu	Asp	Thr	Arg	Leu	Asn	Ile	Asn	Ser	Ser	Pro	Asp	Glu	His
2551	TTTATTGGTG	AGGACACCCG	GCTGAATATT	AATTCCAGTC	CTGATGAGCA	AAATAACCA	TCCTGTGGGC	CGACTTATAA	TTAAGGTCAG	GACTACTCGT							
+1	His	Glu	Pro	Leu	Arg	Arg	Glu	Gln	Gln	Ala	Gly	His	Asp	Glu	Gly	Val	Leu
2601	TGAGCCTTTA	CTGAGACGAG	AGCAACAAGC	TGGCCATGAT	GAAGGTGTT	ACTCGGAAAT	GACTCTGCTC	TCGTTGTTTC	ACCGGTACTA	CTTCCACAAG							
+1	Leu	Asp	Arg	Leu	Val	Asp	Arg	Arg	Glu	Arg	Pro	Leu	Glu	Gly	Gly	Arg	Thr
2651	TGGATCGTCT	TGTGGACAGG	AGGGAACGGC	CACTAGAAGG	TGGCCGAAC	ACCTAGCAGA	ACACCTGTCC	TCCCTTGCCG	GTGATCTTCC	ACCGGCTTGA							
+1	Asn	Ser	Asn	Asn	Asn	Asn	Ser	Asn	Pro	Qs	Ser	Glu	Gln	Asp	Val	Leu	Ala
2701	AATTCCAATA	ACAACAACAG	CAATCCATGT	TCAGAACAAG	ATGTTCTTGC	TTAAGGTTAT	TGTTGTTGTC	GTTAGGTACA	AGTCTTGTTC	TACAAGAACG							
+1	Ala	Gln	Gly	Val	Pro	Ser	Thr	Ala	Ala	Asp	Pro	Gly	Pro	Ser	Lys	Pro	Arg
2751	ACAGGGTGTT	CCAAGCACAG	CAGCAGATCC	TGGGCCATCA	AAGCCCAGAA	TGTCCACAA	GGTTCGTGTC	GTCGTCTAGG	ACCCGGTAGT	TTCGGGTCTT							
+1	Arg	Ala	Gln	Arg	Pro	Asn	Ser	Leu	Asp	Leu	Ser	Ala	Thr	Asn	Val	Leu	Asp
2801	GAGCACAGAG	GCCTAATTCT	CTGGATCTTT	CAGCCACAAA	TGTCCTGGAT	CTCGTGTCTC	CGGATTAAGA	GACCTAGAAA	GTCGGTGTTC	ACAGGACCTA							
+1	Gly	Ser	Ser	Ile	Gln	Ile	Gly	Glu	Ser	Thr	Gln	Asp	Gly	Lys	Ser	Gly	Ser
2851	GGCAGCAGTA	TACAGATAGG	TGAGTCAACA	CAAGATGGCA	AATCAGGATC	CCGTGTCAT	ATGTCTATCC	ACTCAGTTGT	GTCTACCGT	TAGTCCTAG							
+1	Ser	Gly	Glu	Lys	Ile	Lys	Lys	Arg	Val	Lys	Thr	Pro	Tyr	Ser	Leu	Lys	Arg
2901	AGGTGAAAAG	ATCAAGAAAC	GTGTGAAAAC	TCCCTATTCT	CTTAAGCGGT	TCCACTTTTC	TAGTTCTTTG	CACACTTTTG	AGGGATAAGA	GAATTCGCCA							
+1	Trp	Arg	Pro	Ser	Thr	Trp	Val	Ile	Ser	Thr	Glu	Ser	Leu	Asp	Qs	Glu	Val
2951	GGCGCCCCTC	CACCTGGGTC	ATCTCCACTG	AATCGCTGGA	CTGTGAAGTC	CCGCGGGGAG	GTGGACCCAG	TAGAGGTGAC	TTAGCGACCT	GACACTTCAG							
+1	Asn	Asn	Asn	Gly	Ser	Asn	Arg	Ala	Val	His	Ser	Lys	Ser	Ser	Thr	Ala	Val
3001	AACAATAATG	GCAGTAACAG	GGCAGTTCAT	TCCAAATCCA	GCACTGCTGT	TTGTTATTAC	CGTCATTGTC	CCGTCAAGTA	AGGTTTAGGT	CGTGACGACA							
+1	Val	Tyr	Leu	Ala	Glu	Gly	Gly	Thr	Ala	Thr	Thr	Met	Val	Ser	Lys	Asp	Ile
3051	TTACCTTGCA	GAAGGAGGCA	CTGCTACAAC	CATGGTGTCT	AAAGATATAG	AATGGAACGT	CTTCCTCCGT	GACGATGTTG	GTACCACAGA	TTTCTATATC							
+1	Gly	Met	Asn	Qs	Leu	---											
3101	GAATGAACCTG	TCTGTGA															
	CTTACTTGAC	AGACACT															

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